

SEQUENCE LISTING

<110> Ledbetter, Jeffrey

Hayden-Ledbetter, Martha

<120> Binding Domain-Immunoglobulin Fusion Proteins

<130> 390069.401

<140> US

<141> 2002-01-17

<150> US 09/765,208

<151> 2001-01-17

<160> 38

<170> PatentIn version 3.0

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gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg      720
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<223> MURINE ANTI-HUMAN CD20 scFv

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<222> (13)..(807)<223> MOUSE ANTI-HUMAN CD20 SCFV

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<222> (808)..(1513)

<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES
 PROLINE TO SERINE MUTATION (880-883) IN CH2 DISRUPTS EFFECTOR FUNCTION

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<223> HINGE CYSTEINES MUTATED TO SERINES (826-829; 844-847; 853-856)
      WILD TYPE CH2 AND CH3 DOMAINS MEDIATE EFFECTOR FUNCTIONS
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<223> LIGHT CHAIN LEADER PEPTIDE

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<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

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<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

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<223> BclI restriction site

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aagcctggga cttcagtga gctgtcctgc aaggcctctg gctacacctt caccaactac	540
tggatggtct ggggtgaagca gacgcctgga gaaggccttg agtggattgg agaaattatt	600
cctagcaacg gtcgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca	660
gacaaatcct cccgcacagc ctacatgcaa ctacagagcc tggcatctga ggactctgcg	720
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggtttgctt	780
actggggcca agggactctg gtcactgtct ctgcagcctg atca	824

<210> 11

<211> 266

<212> PRT

<213> Mus musculus

<220>

<221> INIT_MET

<222> (1)..(1)

<220>

<221> SIGNAL

<222> (1)..(22)

<220>

<221> DOMAIN

<222> (23)..(128)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<220>

<221> SITE

<222> (129)..(144)

<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE

<220>

<221> DOMAIN

<222> (145)..(266)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<400> 11

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20				25						30		

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
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50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp
 260 265

<210> 12

<211> 271

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(271)

<223> MOUSE ANTI-HUMAN CD19 SCFV

20250504

<400> 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 35 40 45
 Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 50 55 60
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 65 70 75 80
 Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95
 Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 100 105 110
 Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125
 Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140
 Gly Ser Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 145 150 155 160
 Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
 165 170 175
 Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 180 185 190
 Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn
 195 200 205
 Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser
 210 215 220
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
 225 230 235 240
 Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr
 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 260 265 270

<210> 13

<211> 259

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(259)

<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met	Val	Ser	Thr	Ala	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Thr
1				5					10					15	

Gly	Gly	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser
			20					25					30		

Ala	Ser	Val	Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	Glu	Asn
		35					40					45			

Val	Tyr	Ser	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro
	50					55					60				

Gln	Leu	Leu	Val	Ser	Phe	Ala	Lys	Thr	Leu	Ala	Glu	Gly	Val	Pro	Ser
65					70					75					80

Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ser	Leu	Lys	Ile	Ser
				85					90					95	

Ser	Leu	Gln	Pro	Glu	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Gln	His	His	Ser
			100					105					110		

Asp	Asn	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Glu	Leu	Glu	Ile	Lys	Gly
		115					120					125			

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ala
		130				135						140			

Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Glu	Lys	Pro	Gly	Ala	Ser
145					150					155					160

Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	Asn
				165					170					175	

Met	Asn	Trp	Val	Lys	Gln	Asn	Asn	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly
			180					185					190		

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
210 215 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
245 250 255

Val Ser Ser

<210> 14

<211> 272

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(272)

<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser
35 40 45

Val Phe Tyr Ser Ser Asn Gln Arg Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val His Thr Glu Asp Leu Ala Val Tyr
100 105 110

Tyr Cys His Gln Phe Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys
 115 120 125
 Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val
 145 150 155 160
 Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 165 170 175
 Phe Thr Asn Tyr Trp Met Val Trp Val Lys Gln Thr Pro Gly Glu Gly
 180 185 190
 Leu Glu Trp Ile Gly Glu Ile Ile Pro Ser Asn Gly Arg Thr Lys Tyr
 195 200 205
 Asn Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 210 215 220
 Arg Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala
 225 230 235 240
 Val Tyr Tyr Cys Ala Arg Glu Met Ser Ile Ile Thr Thr Val Leu Thr
 245 250 255
 Pro Gly Leu Leu Thr Gly Ala Lys Gly Leu Trp Ser Leu Ser Leu Gln
 260 265 270

<210> 15

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125

Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220

Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225					230					235					240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys

260					265					270					
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
		275					280					285			
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
	290					295					300				
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
305					310					315					320
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
				325					330					335	
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
			340					345					350		
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
			355				360					365			
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
	370					375					380				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
385					390					395					400
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
			405					410						415	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
			420				425						430		
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
		435					440					445			
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
	450					455					460				
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
465					470					475					480
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
			485					490						495	

Pro Gly Lys

<210> 16

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>

<221> DOMAIN

<222> (265)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
		50				55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70						75				80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135				140					
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145					150					155					160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
 260 265 270
 Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 17

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
 CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
 260 265 270
 Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(288)

<223> WILD TYPE IGA HINGE

CD20-SCFV

<220>

<221> DOMAIN

<222> (289)..(505)

<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1          5          10          15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20          25          30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35          40          45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50          55          60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65          70          75          80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85          90          95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100         105         110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115         120         125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130         135         140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145         150         155         160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165         170         175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180         185         190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195         200         205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210         215         220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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225		230		235		240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp						
		245		250		255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr						
		260		265		270
Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys						
		275		280		285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys						
		290		295		300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val						
		305		310		315
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr						
		325		330		335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu						
		340		345		350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His						
		355		360		365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys						
		370		375		380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln						
		385		390		395
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu						
		405		410		415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro						
		420		425		430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn						
		435		440		445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu						
		450		455		460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val						
		465		470		475
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln						
		485		490		495
Lys Ser Leu Ser Leu Ser Pro Gly Lys						
		500		505		

<210> 19

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)
WILD TYPE CH2 AND CH3 DOMAINS
ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp	Gln	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	1	5	10	15
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	20	25	30	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	35	40	45	
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	50	55	60	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	65	70	75	80
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	85	90	95	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	100	105	110	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	115	120	125	
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	130	135	140	
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	145	150	155	160
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	165	170	175	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	180	185	190	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	195	200	205	

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 20

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)..(23)

<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>

<221> DOMAIN

<222> (24)..(240)

<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser
 20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 50 55 60

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 65 70 75 80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 85 90 95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 100 105 110

SCFVIG FUSION PROTEINS

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 115 120 125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 130 135 140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 145 150 155 160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 165 170 175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 180 185 190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 195 200 205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 210 215 220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230 235 240

<210> 21

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (1)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1455)

<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
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 ccaggggaga aggtcacaaat gacttgacag gccagctcaa gtgtaagtta catgcaactg 180
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
 tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc 300
 agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgg 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
 aggctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggcacaggga ccacggtcac cgtctctgat ccaagaagg tggacaagat agaagatgaa 840
 aggaatcttc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa 900
 agatccttat ccttactgaa ctgtgaggag attaaaagcc agtttgaagg ctttgtgaag 960
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 ccttgcgggc aacaatccat tcaactggga ggagtatttg aattgcaacc aggtgcttcg 1380
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<210> 22

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (13)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1275)

<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22

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gtcataattg ccagaggaca aattgttctc tcccagtctc cagcaatcct gtctgcatct      120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg      180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct      240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc      300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaacca      360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg      420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggg      480
aggcctgggg cctcagtgaat gatgtcctgc aaggcttctg gctacacatt taccagttac      540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat      600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta      660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg      720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg      780

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ggcacagggg ccacgggtcac cgtctctgat ccagaaaaca gctttgaaat gcaaaaaggt 840
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gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggg aaccctggaa 960
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tcccccggtg gattcgagag aatcttactc agagctgcaa ataccacag ttccgcaaaa 1140
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gtgtttgtca atgtgactga tccaagccaa gtgagccatg gactggctt cacgtccttt 1260
ggcttactca aactcgagtg ataatctaga 1290

<210> 23

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 23
gtcaagcttg ccgcatgga ttttcaagtg cagatttttc agc

43

<210> 24

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 24
gtcgtcgagc tcccacctcc tccagatcca ccaccgccg agccaccgcc acctttcagc

60

20250906095004

tccagcttgg tccc

74

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 25

gctgctgagc tctcaggctt atctacagca agtctgg

37

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 26

gttgtctgat cagagacggt gaccgtggtc cc

32

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 27

34

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

44

<210> 29

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

35

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 30

gtctatataa gcagagctct ggc

23

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 31

cgaggctgat cagcgagctc tagca

25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 32

ccgcaatttg aggattctga tcacc

25

<210> 33

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(266)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> DOMAIN

<222> (268)..(481)

<223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe

EXCELLENCE

195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
 260 265 270
 Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
 275 280 285
 Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
 290 295 300
 Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
 305 310 315 320
 Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
 325 330 335
 Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
 340 345 350
 Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
 355 360 365
 Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
 370 375 380
 Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
 385 390 395 400
 Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
 405 410 415
 Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
 420 425 430
 Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
 435 440 445
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
 450 455 460
 Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
 465 470 475 480
 Leu Glu

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<210> 34
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE
 <222> (1)..(266)
 <223> MOUSE ANTI-HUMAN SCFV

<220>

<221>
 DOMAIN
 <222> (268)..(421)
 <223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
	50					55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65					70				75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100				105						110		

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Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
 260 265 270
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 290 295 300
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 305 310 315 320
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 325 330 335
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 340 345 350
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 355 360 365
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 370 375 380
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 385 390 395 400
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 405 410 415

Gly Leu Leu Lys Leu Glu
420

<210> 35

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<221> N_region

<222> (1)..(63)

<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35

ccagttccct caactccacc taccocatct ccctcaactc cacctacccc atctccctca 60

tgc 63

<210> 36

<211> 21

<212> PRT

<213> Homo sapiens

<400> 36

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
1 5 10 15

Pro Ser Pro Ser Cys
20

<210> 37

<211> 763

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(6)

<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>

<221> N_region

<222> (8)..(752)

<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37
 tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60
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 aggttcagaa gcgatacctca cgtgcacact gaccggcctg agagatgcct caggtgtcac 180
 ctacacctgg acgccctcaa gtgggaagag cgctgttcaa ggaccacctg accgtgacct 240
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 ctcaaaatcc ggaaacacat tccggcccga ggtccacctg ctgccgccgc cgtcggagga 420
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 cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattggtg gccacgaggc 660
 cctgccgctg gccttcacac agaagaccat cgaccgcttg gcgggtaaac ccacccatgt 720
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<210> 38

<211> 250

<212> PRT

<213> Homo sapiens

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<221> DOMAIN
<222> (3)..(250)
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50 55 60

Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
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Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
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Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100 105 110

Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115 120 125

Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130 135 140

Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145 150 155 160

Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
165 170 175

Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
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Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
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Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
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Asn Val Ser Val Val Met Ala Glu Val Asp
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